

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yi Li and Mark D. Adams
- (ii) TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: NJ
 - (E) COUNTRY: US
 - (F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/465,971
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MULLINS, J.G.
 - (B) REGISTRATION NUMBER: 33073
 - (C) REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTACAGGT AACATTCTGA AATTGAACTA AACAGTAAAT TCTGTTGAAA TGTTTTTCAAA	60
GAGGCAAAAT ATTATATTGG AATCAATGAA GAAAGTAAAT TATCTTGGCT AATTTTATTA	120
GTGGTAATTG TAGTGAAAGG TTTCCTTAAA TATTATAAGC AAATTCCTTT TCTCCCCCGT	180
CTCAAATGAA AGGAAATGGG GGTAAATTAA TCTGACTGTG ATTGGTTTTG TTTTATGCTG	240
ATCTTGAAAG CTTGATGTTG CTGCTGCTCC TCATACAGTA CAGATCAGTT GTGTGGGGTG	300
CTATTGAGGG TAGCCGTGAA TAGTGGTGCC AGTAGGGGTG GAGCGGGAGG GATGATGCCA	360
GCCTGAGCTA GCCAGGTTCT TTGATTAGGG CATTGGATGT GAAATGTAAA ATGCTCTCTC	420
CTTTCTTCT ATCAGCTGTT CAGAGGAGAC TCATTACAAC TCCTGCTGAA GCTCCTAATC	480
TTCTTCCCTT CTCTTCTACC CTTTCCCCCT ACCCTCACTT GGCCTGAAGA CGTTCTCCCC	540
AGAGTTTACC TTGCTCCCCT GGTGCTATGT GTATGGTGAA CCTGGCACTA TGGCCGCGTC	600
TGGGACTGGC CAGACAACTG CTGCTGGCTC TCCTTATTCC AGGAAGGATT TAAAGGGGAA	660
TTGCACTGCA GGCAATGCAC CAGAGCAGCA GCATCAGGAG CTTGGGGAGT AAGGCTCCTC	720
TGGCATTATT ACACACATGC AAAGCTGACC GCAATGACAG CAGCTGCTTC TTTGAACTGT	780
TGGCAGCAGC CAAGCGGCAG CATGAAGTGA CAGATCACTC CTGAGCTCAA G ATG AAC	837
	Met Asn
TCC ACC TTG GAT GGT AAT CAG AGC AGC CAC CCT TTT TGC CTC TTG GCA	885
Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu Leu Ala	
5 10 15	
TTT GGC TAT TTG GAA ACT GTC AAT TTT TGC CTT TTG GAA GTA TTG ATT	933
Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val Leu Ile	
20 25 30	
ATT GTC TTT CTA ACT GTA TTG ATT ATT TCT GGC AAC ATC ATT GTG ATT	981
Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile Val Ile	
35 40 45 50	
TTT GTA TTT CAC TGT GCA CCT TTG TTG AAC CAT CAC ACT ACA AGT TAT	1029
Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr Ser Tyr	
55 60 65	
TTT ATC CAG ACT ATG GCA TAT GCT GAC CTT TTT GTT GGG GTG AGC TGC	1077
Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val Ser Cys	
70 75 80	
GTG GTC CCT TCT TTA TCA CTC CTC CAT CAC CCC CTT CCA GTA GAG GAG	1125
Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val Glu Glu	
85 90 95	
TCC TTG ACT TGC CAG ATA TTT GGT TTT GTA GTA TCA GTT CTG AAG AGC	1173
Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu Lys Ser	
100 105 110	
GTC TCC ATG GCT TCT CTG GCC TGT ATC AGC ATT GAT AGA TAC ATT GCC	1221
Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr Ile Ala	
115 120 125 130	

ATT	ACT	AAA	CCT	TTA	ACC	TAT	AAT	ACT	CTG	GTT	ACA	CCC	TGG	AGA	CTA		1269
Ile	Thr	Lys	Pro	Leu	Thr	Tyr	Asn	Thr	Leu	Val	Thr	Pro	Trp	Arg	Leu		
			135						140					145			
CGC	CTG	TGT	ATT	TTC	CTG	ATT	TGG	CTA	TAC	TCG	ACC	CTG	GTC	TTC	CTG		1317
Arg	Leu	Cys	Ile	Phe	Leu	Ile	Trp	Leu	Tyr	Ser	Thr	Leu	Val	Phe	Leu		
			150						155				160				
CCT	TCC	TTT	TTC	CAC	TGG	GGC	AAA	CCT	GGA	TAT	CAT	GGA	GAT	GTG	TTT		1365
Pro	Ser	Phe	Phe	His	Trp	Gly	Lys	Pro	Gly	Tyr	His	Gly	Asp	Val	Phe		
		165					170					175					
CAG	TGG	TGT	GCG	GAG	TCC	TGG	CAC	ACC	GAC	TCC	TAC	TTC	ACC	CTG	TTC		1413
Gln	Trp	Cys	Ala	Glu	Ser	Trp	His	Thr	Asp	Ser	Tyr	Phe	Thr	Leu	Phe		
	180					185					190						
ATC	GTG	ATG	ATG	TTA	TAT	GCC	CCA	GCA	GCC	CTT	ATT	GTC	TGC	TTC	ACC		1461
Ile	Val	Met	Met	Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys	Phe	Thr		
195					200					205					210		
TAT	TTC	AAC	ATC	TTC	CGC	ATC	TGC	CAA	CAG	CAC	ACA	AAG	GAT	ATC	AGC		1509
Tyr	Phe	Asn	Ile	Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp	Ile	Ser		
				215					220					225			
GAA	AGG	CAA	GCC	CGC	TTC	AGC	AGC	CAG	AGT	GGG	GAG	ACT	GGG	GAA	GTG		1557
Glu	Arg	Gln	Ala	Arg	Phe	Ser	Ser	Gln	Ser	Gly	Glu	Thr	Gly	Glu	Val		
			230					235					240				
CAG	GCC	TGT	CCT	GAT	AAG	CGC	TAT	GCC	ATG	GTC	CTG	TTT	CGA	ATC	ACT		1605
Gln	Ala	Cys	Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg	Ile	Thr		
		245					250					255					
AGT	GTA	TTT	TAC	ATC	CTC	TGG	TTG	CCA	TAT	ATC	ATC	TAC	TTC	TTG	TTG		1653
Ser	Val	Phe	Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe	Leu	Leu		
	260					265					270						
GAA	AGC	TCC	ACT	GGC	CAC	AGC	AAC	CGC	TTC	GCA	TCC	TTC	TTG	ACC	ACC		1701
Glu	Ser	Ser	Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu	Thr	Thr		
275					280				285						290		
TGG	CTT	GCT	ATT	AGT	AAC	AGT	TTC	TGC	AAC	TGT	GTA	ATT	TAT	AGT	CTC		1749
Trp	Leu	Ala	Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr	Ser	Leu		
				295				300						305			
TCC	AAC	AGT	GTA	TTC	CAA	AGA	GGA	CTA	AAG	CGC	CTC	TCA	GGG	GCT	ATG		1797
Ser	Asn	Ser	Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly	Ala	Met		
			310					315					320				
TGT	ACT	TCT	TGT	GCA	AGT	CAG	ACT	ACA	GCC	AAC	GAC	CCT	TAC	ACA	GTT		1845
Cys	Thr	Ser	Cys	Ala	Ser	Gln	Thr	Thr	Ala	Asn	Asp	Pro	Tyr	Thr	Val		

ACTCAAGATC ATGAAGACAA ATTGCTCTTG CTCTCAATTT TTGAAATGTC TTGGAAATGA 2138
 CTACAGTTCT CAGATTTAAA ATGAATAAAG CCATATCTAA CACCTCTTTC CAGCTGGCAT 2198
 GACTGAACCT GAGTGTGAAA AGCGTCAGCA TTTTAAAAAG TCATCACTTT CTTGTCACCTT 2258
 TCTGGGCTCT TTCCAGCTAT TTGGGCGTCA TATGCAATTG ATTTCTTCTA ACGGAATAGT 2318
 AAAATATAAA TGAAAAGGTT TTAGAAATTA CTTTTTATGT ATGCCAAAGC ATAACTACAC 2378
 TGCAAGTTTC AACACTGTCA TTTAGAAAGC CAAATGTTCT GTGTTTTATT CTCTTGAGAG 2438
 AATTCTCAGT AGGGTGAATA ATGTGAACAC ATAAACATTA ATTTTAGAAT TTTACAGTGA 2498
 ACCATGAAGC AAAAGTGCAA TCAAATTATA CAATTTATGA AAAACTGAGC TACTTTTTGT 2558
 GCCATGCTTC ACAGAGATCT AAAGATATGT GTGCGTAGAA GTAATCGTGT AGTACTTTTG 2618
 CCCATGCCTT TGTGTTATGT CTATATTTAG AATATCTGAA TTGTTAGATT TCTCTTTTAC 2678
 AGCAAAATGT GCTTAAGCTA AAAAGTAATT CAGGGAATTC GATATCAAGC TTATCGATAC 2738
 CGTCGACCTC GAGGGGGGGC CCGGTA 2764

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Ser	Thr	Leu	Asp	Gly	Asn	Gln	Ser	Ser	His	Pro	Phe	Cys	Leu
				5					10					15	
Leu	Ala	Phe	Gly	Tyr	Leu	Glu	Thr	Val	Asn	Phe	Cys	Leu	Leu	Glu	Val
			20					25					30		
Leu	Ile	Ile	Val	Phe	Leu	Thr	Val	Leu	Ile	Ile	Ser	Gly	Asn	Ile	Ile
			35				40					45			
Val	Ile	Phe	Val	Phe	His	Cys	Ala	Pro	Leu	Leu	Asn	His	His	Thr	Thr
	50					55					60				
Ser	Tyr	Phe	Ile	Gln	Thr	Met	Ala	Tyr	Ala	Asp	Leu	Phe	Val	Gly	Val
	65				70					75				80	
Ser	Cys	Val	Val	Pro	Ser	Leu	Ser	Leu	Leu	His	His	Pro	Leu	Pro	Val
				85					90					95	
Glu	Glu	Ser	Leu	Thr	Cys	Gln	Ile	Phe	Gly	Phe	Val	Val	Ser	Val	Leu
			100					105					110		
Lys	Ser	Val	Ser	Met	Ala	Ser	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr
		115					120					125			
Ile	Ala	Ile	Thr	Lys	Pro	Leu	Thr	Tyr	Asn	Thr	Leu	Val	Thr	Pro	Trp
	130					135					140				
Arg	Leu	Arg	Leu	Cys	Ile	Phe	Leu	Ile	Trp	Leu	Tyr	Ser	Thr	Leu	Val
	145				150					155				160	
Phe	Leu	Pro	Ser	Phe	Phe	His	Trp	Gly	Lys	Pro	Gly	Tyr	His	Gly	Asp
				165					170					175	
Val	Phe	Gln	Trp	Cys	Ala	Glu	Ser	Trp	His	Thr	Asp	Ser	Tyr	Phe	Thr
			180					185						190	

Leu	Phe	Ile	Val	Met	Met	Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys
		195					200					205			
Phe	Thr	Tyr	Phe	Asn	Ile	Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp
	210					215					220				
Ile	Ser	Glu	Arg	Gln	Ala	Arg	Phe	Ser	Ser	Gln	Ser	Gly	Glu	Thr	Gly
225					230					235					240
Glu	Val	Gln	Ala	Cys	Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg
				245					250					255	
Ile	Thr	Ser	Val	Phe	Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe
			260					265					270		
Leu	Leu	Glu	Ser	Ser	Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu
		275					280					285			
Thr	Thr	Trp	Leu	Ala	Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr
	290					295					300				
Ser	Leu	Ser	Asn	Ser	Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly
305					310					315					320
Ala	Met	Cys	Thr	Ser	Cys	Ala	Ser	Gln	Thr	Thr	Ala	Asn	Asp	Pro	Tyr
				325					330					335	
Thr	Val	Arg	Ser	Lys	Gly	Pro	Leu	Asn	Gly	Cys	His	Ile			
			340					345							

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asn	Ser	Thr	Leu	Xaa	Asp	Gly	Asn	Gln	Ser	Ser	His	Pro	Phe	Cys
				5					10					15	
Leu	Leu	Ala	Phe	Gly	Tyr	Leu	Glu	Thr	Val	Asn	Phe	Cys	Leu	Leu	Glu
		20						25					30		
Val	Leu	Ile	Val	Xaa	Xaa	Xaa	Xaa	Phe	Leu	Thr	Val	Leu	Ile	Ile	
		35					40				45				
Ser	Gly	Asn	Ile	Ile	Val	Ile	Phe	Val	Phe	His	Cys	Ala	Pro	Leu	Leu
	50					55				60					
Asn	His	His	Thr	Thr	Ser	Tyr	Phe	Ile	Gln	Thr	Met	Ala	Tyr	Ala	Asp
65					70					75				80	
Leu	Phe	Val	Gly	Val	Ser	Cys	Val	Val	Pro	Ser	Leu	Ser	Leu	Leu	His
				85					90					95	
His	Pro	Leu	Pro	Xaa	Xaa	Val	Glu	Glu	Ser	Leu	Thr	Cys	Gln	Ile	Phe
			100					105					110		
Gly	Phe	Val	Val	Ser	Val	Leu	Lys	Ser	Val	Ser	Met	Ala	Ser	Leu	Ala
		115					120					125			
Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Ile	Ala	Ile	Thr	Lys	Pro	Leu	Thr	Tyr
	130					135					140				
Asn	Thr	Leu	Val	Thr	Pro	Trp	Arg	Leu	Arg	Leu	Cys	Ile	Phe	Leu	Ile
145					150					155					160
Trp	Leu	Tyr	Ser	Thr	Leu	Val	Phe	Leu	Pro	Ser	Phe	Phe	His	Trp	Gly
			165						170					175	
Lys	Pro	Gly	Tyr	His	Gly	Asp	Val	Phe	Gln	Trp	Cys	Ala	Glu	Ser	Trp
			180					185					190		
Xaa	Xaa	Xaa	His	Thr	Asp	Ser	Tyr	Phe	Thr	Leu	Phe	Ile	Val	Met	Met
			195				200					205			

Leu	Tyr	Ala	Pro	Ala	Ala	Leu	Ile	Val	Cys	Phe	Thr	Tyr	Phe	Asn	Ile
210						215					220				
Phe	Arg	Ile	Cys	Gln	Gln	His	Thr	Lys	Asp	Ile	Ser	Glu	Arg	Xaa	Xaa
225				230					235						240
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Ala	Arg	Phe	Ser
			245						250					255	
Ser	Gln	Ser	Gly	Xaa	Xaa	Xaa	Xaa	Glu	Thr	Gly	Glu	Val	Gln	Ala	Cys
			260					265					270		
Pro	Asp	Lys	Arg	Tyr	Ala	Met	Val	Leu	Phe	Arg	Ile	Thr	Ser	Val	Phe
		275					280					285			
Tyr	Ile	Leu	Trp	Leu	Pro	Tyr	Ile	Ile	Tyr	Phe	Leu	Leu	Glu	Ser	Ser
	290					295					300				
Thr	Gly	His	Ser	Asn	Arg	Phe	Ala	Ser	Phe	Leu	Thr	Thr	Trp	Leu	Ala
305				310					315						320
Ile	Ser	Asn	Ser	Phe	Cys	Asn	Cys	Val	Ile	Tyr	Ser	Leu	Ser	Asn	Ser
			325						330					335	
Val	Phe	Gln	Arg	Gly	Leu	Lys	Arg	Leu	Ser	Gly	Ala	Met	Cys	Thr	Ser
			340					345					350		
Cys	Ala	Ser	Gln	Thr	Thr										
		355													

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Ser	Leu	Gln	Pro	Asp	Ala	Gly	Asn	Ala	Ser	Trp	Asn	Gly	Thr
			5						10					15	
Glu	Ala	Pro	Gly	Gly	Ala	Arg	Ala	Thr	Pro	Tyr	Ser	Leu	Gln	Val	
		20					25					30			
Thr	Leu	Thr	Leu	Val	Cys	Leu	Ala	Gly	Leu	Leu	Met	Leu	Leu	Thr	Val
		35					40					45			
Phe	Gly	Asn	Val	Leu	Val	Ile	Ile	Ala	Val	Phe	Thr	Ser	Arg	Ala	Leu
	50				55					60					
Lys	Ala	Pro	Gln	Asn	Leu	Phe	Leu	Val	Xaa	Ser	Leu	Ala	Ser	Ala	Asp
	65			70					75					80	
Ile	Leu	Val	Ala	Xaa	Xaa	Thr	Leu	Val	Ile	Pro	Phe	Ser	Leu	Ala	Asn
			85					90						95	
Glu	Val	Met	Gly	Tyr	Trp	Tyr	Phe	Gly	Lys	Ala	Trp	Cys	Glu	Ile	Tyr
		100						105					110		
Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	Thr	Ser	Ser	Ile	Val	His	Leu	Cys
		115					120					125			
Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	Ser	Ile	Thr	Gln	Ala	Ile	Glu	Tyr
	130				135					140					
Asn	Leu	Lys	Arg	Thr	Pro	Arg	Arg	Ile	Lys	Ala	Ile	Ile	Ile	Thr	Val
	145				150					155				160	
Trp	Val	Ile	Ser	Ala	Val	Ile	Ser	Phe	Pro	Pro	Leu	Ile	Ser	Ile	Glu
			165					170					175		
Lys	Lys	Gly	Xaa	Xaa	Gly	Gly	Gly	Gly	Pro	Gln	Pro	Ala	Glu	Pro	Arg
		180					185						190		
Cys	Glu	Ile	Asn	Asp	Gln	Lys	Trp	Tyr	Val	Ile	Ser	Ser	Cys	Ile	Gly
	195					200					205				
Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr	Val	Arg	Ile
	210					215					220				

Tyr	Gln	Ile	Ala	Lys	Arg	Arg	Thr	Arg	Val	Pro	Pro	Ser	Arg	Arg	Gly
225					230					235					240
Pro	Asp	Ala	Val	Ala	Ala	Pro	Pro	Gly	Gly	Leu	Gln	Gly	Arg	Gly	Arg
				245					250					255	
Ser	Ala	Ser	Gly	Leu	Pro	Arg	Arg	Arg	Ala	Gly	Ala	Gly	Gly	Gln	Asn
			260					265					270		
Arg	Glu	Lys	Arg	Phe	Thr	Phe	Val	Leu	Ala	Val	Val	Ile	Gly	Val	Phe
		275					280					285			
Val	Val	Cys	Trp	Phe	Pro	Phe	Phe	Phe	Thr	Tyr	Thr	Leu	Thr	Ala	Val
	290					295					300				
Gly	Cys	Ser	Val	Pro	Arg	Thr	Leu	Phe	Lys	Phe	Phe	Phe	Trp	Phe	Gly
305					310					315					320
Tyr	Cys	Asn	Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Ile	Phe	Asn	His
			325						330					335	
Asp	Phe	Arg	Arg	Ala	Phe	Lys	Lys	Ile	Xaa	Xaa	Xaa	Leu	Cys	Arg	Gly
			340					345					350		
Asp	Arg	Lys	Arg	Ile	Val										
		355													

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGAATTCCT CCATGAACTC CACCTTGGAT

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAAGCTTC GTCAGATATG ACATCCATT

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCAAGCTT GCCACCATGA ACTCCACCTT GGAT

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTCGAG TCAAGCGTAC TCTGGGACGT CGTATGGGTA GCAGATATGA CATCCATTAA

50

G

61

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCCT CCATGAACTC CACCTTGGAT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCCG CTCAGATATG AGATCCATT

29